



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/996,611A  
Source: OTPE  
Date Processed by STIC: 5/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/996,611A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence
- 11 ☐ Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

## RAW SEQUENCE LISTING

DATE: 05/14/2002

PATENT APPLICATION: US/09/996,611A

TIME: 15:50:52

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\05142002\I996611A.raw

Does Not Comply  
Corrected Diskette Needed

pp1-7

1 <110> APPLICANT: Chou, Min-Yuan  
 2 Leu, Charng-Yih  
 4 <120> TITLE OF INVENTION: Novel Human alpha 1 Chain Collagen  
 6 <130> FILE REFERENCE: 32350-176844  
 8 <140> CURRENT APPLICATION NUMBER: US 09/996,611A  
 9 <141> CURRENT FILING DATE: 2001-11-30  
 11 <150> PRIOR APPLICATION NUMBER: TAIWAN 89128027  
 12 <151> PRIOR FILING DATE: 2000-12-27  
 14 <160> NUMBER OF SEQ ID NOS: 5  
 16 <170> SOFTWARE: Microsoft Word

## ERRORED SEQUENCES

18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 954  
 20 <212> TYPE: PRT  
 21 <213> ORGANISM: Homo sapiens  
 23 <220> FEATURE:  
 24 <223> OTHER INFORMATION: alpha 1 chain collagen  
 25 Pro in this sequence stands for hydroxyproline  
 27 <400> SEQUENCE: 1  
 28 Met Ala His Tyr Ile Thr Phe Leu Cys Met Val Leu Val Leu Leu  
 E--> 29 1 5 10 15  
 30 Leu Gln Asn Ser Val Leu Ala Glu Asp Gly Glu Val Arg Ser Ser  
 E--> 31 20 25 30  
 32 Cys Arg Thr Ala Pro Thr Asp Leu Val Phe Ile Leu Asp Gly Ser  
 E--> 33 35 40 45  
 34 Tyr Ser Val Gly Pro Glu Asn Phe Glu Ile Val Lys Lys Trp Leu  
 E--> 35 50 55 60  
 36 Val Asn Ile Thr Lys Asn Phe Asp Ile Gly Pro Lys Phe Ile Gln  
 E--> 37 65 70 75  
 38 Val Gly Val Val Gln Tyr Ser Asp Tyr Pro Val Leu Glu Ile Pro  
 E--> 39 80 85 90  
 40 Leu Gly Ser Tyr Asp Ser Gly Glu His Leu Thr Ala Ala Val Glu  
 E--> 41 95 100 105  
 42 Ser Ile Leu Tyr Leu Gly Gly Asn Thr Lys Thr Gly Lys Ala Ile  
 E--> 43 110 115 120  
 44 Gln Phe Ala Leu Asp Tyr Leu Phe Ala Lys Ser Ser Arg Phe Leu  
 E--> 45 125 130 135  
 46 Thr Lys Ile Ala Val Val Leu Thr Asp Gly Lys Ser Gln Asp Asp  
 E--> 47 140 145 150  
 48 Val Lys Asp Ala Ala Gln Ala Ala Arg Asp Ser Lys Ile Thr Leu

misaligned  
 amino acid  
 number  
 (see item 3 on  
 Err Summary  
 sheet)

## RAW SEQUENCE LISTING

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\05142002\I996611A.raw

```

E--> 49 155 160 165
50 Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp Ala Glu Leu Arg
E--> 51 170 175 180
52 Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe Tyr Val Glu
E--> 53 185 190 195
54 Asp Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met Lys Gln Lys
E--> 55 200 205 210
56 Leu Cys Glu Glu Ser Val Cys Pro Thr Arg Ile Pro Val Ala Ala
E--> 57 215 220 225
58 Arg Asp Glu Arg Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn
E--> 59 230 235 240
60 Lys Lys Val Lys Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys
E--> 61 245 250 255
62 Gly Tyr Glu Val Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser
E--> 63 260 265 270
64 Asn Val Phe Pro Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser
E--> 65 275 280 285
66 Thr Gln Arg Phe Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile
E--> 67 290 295 300
68 Leu Thr Ile Asp Gly Arg Pro Gln Ile Ala Val Thr Leu Asn Gly
E--> 69 305 310 315
70 Val Asp Lys Ile Leu Leu Phe Thr Thr Thr Ser Val Ile Asn Gly
E--> 71 320 325 330
72 Ser Gln Val Val Thr Phe Ala Asn Pro Gln Val Lys Thr Leu Phe
E--> 73 335 340 345
74 Asp Glu Gly Trp His Gln Ile Arg Leu Leu Val Thr Glu Gln Asp
E--> 75 350 355 360
76 Val Thr Leu Tyr Ile Asp Asp Gln Gln Ile Glu Asn Lys Pro Leu
E--> 77 365 370 375
78 His Pro Val Leu Gly Ile Leu Ile Asn Gly Gln Thr Gln Ile Gly
E--> 79 380 385 390
80 Lys Tyr Ser Gly Lys Glu Glu Thr Val Gln Phe Asp Val Gln Lys
E--> 81 395 400 405
82 Leu Arg Ile Tyr Cys Asp Pro Glu Gln Asn Asn Arg Glu Thr Ala
E--> 83 410 415 420
84 Cys Glu Ile Pro Gly Phe Cys Leu Asn Gly Pro Ser Asp Val Gly
E--> 85 425 430 435
86 Ser Thr Pro Ala Pro Cys Ile Cys Pro Pro Gly Lys Pro Gly Leu
E--> 87 440 445 450
88 Gln Gly Pro Lys Gly Asp Pro Gly Leu Pro Gly Asn Pro Gly Tyr
E--> 89 455 460 465
90 Pro Gly Gln Pro Gly Gln Asp Gly Lys Pro Gly Tyr Gln Gly Ile
E--> 91 470 475 480
92 Ala Gly Thr Pro Gly Val Pro Gly Ser Pro Gly Ile Gln Gly Ala
E--> 93 485 490 495
94 Arg Gly Leu Pro Gly Tyr Lys Gly Glu Pro Gly Arg Asp Gly Asp
E--> 95 500 505 510
96 Lys Gly Asp Arg Gly Leu Pro Gly Phe Pro Gly Leu His Gly Met
E--> 97 515 520 525

```

*see  
item 3  
on Enol  
Summary  
Sheet*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/996,611A

DATE: 05/14/2002  
TIME: 15:50:52

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF3\05142002\I996611A.raw

98 Pro Gly Ser Lys Gly Glu Met Gly Ala Lys Gly Asp Lys Gly Ser  
E--> 99 530 535 540  
100 Pro Gly Phe Tyr Gly Lys Lys Gly Ala Lys Gly Glu Lys Gly Asn  
E--> 101 545 550 555  
102 Ala Gly Phe Pro Gly Leu Pro Gly Pro Ala Gly Glu Pro Gly Arg  
E--> 103 560 565 570  
104 His Gly Lys Asp Gly Leu Met Gly Ser Pro Gly Phe Lys Gly Glu  
E--> 105 575 580 585  
106 Ala Gly Ser Pro Gly Ala Pro Gly Gln Asp Gly Thr Arg Gly Glu  
E--> 107 590 595 600  
108 Pro Gly Ile Pro Gly Phe Pro Gly Asn Arg Gly Leu Met Gly Gln  
E--> 109 605 610 615  
110 Lys Gly Glu Ile Gly Pro Pro Gly Gln Gln Gly Lys Lys Gly Ala  
E--> 111 620 625 630  
112 Pro Gly Met Pro Gly Leu Met Gly Ser Asn Gly Ser Pro Gly Gln  
E--> 113 635 640 645  
114 Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys Gly Glu Pro Gly Ile  
E--> 115 650 655 660  
116 Gln Gly Met Pro Gly Ala Ser Gly Leu Lys Gly Glu Pro Gly Ala  
E--> 117 665 670 675  
118 Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met Gly Leu Pro Gly Ile  
E--> 119 680 685 690  
120 Gln Gly Lys Lys Gly Asp Lys Gly Asn Gln Gly Glu Lys Gly Ile  
E--> 121 695 700 705  
122 Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln Gly Ile Pro Gly Gln  
E--> 123 710 715 720  
124 Gln Gly Ile Gln Gly His His Gly Ala Lys Gly Glu Arg Gly Glu  
E--> 125 725 730 735  
126 Lys Gly Glu Pro Gly Val Arg Gly Ala Ile Gly Ser Lys Gly Glu  
E--> 127 740 745 750  
128 Ser Gly Val Asp Gly Leu Met Gly Pro Ala Gly Pro Lys Gly Gln  
E--> 129 755 760 765  
130 Pro Gly Asp Pro Gly Pro Gln Gly Pro Pro Gly Leu Asp Gly Lys  
E--> 131 770 775 780  
132 Pro Gly Arg Glu Phe Ser Glu Gln Phe Ile Arg Gln Val Cys Thr  
E--> 133 785 790 795  
134 Asp Val Ile Arg Ala Gln Leu Pro Val Leu Leu Gln Ser Gly Arg  
E--> 135 800 805 810  
136 Ile Arg Asn Cys Asp His Cys Leu Ser Gln His Gly Ser Pro Gly  
E--> 137 815 820 825  
138 Ile Pro Gly Pro Pro Gly Pro Ile Gly Pro Glu Gly Pro Arg Gly  
E--> 139 830 835 840  
140 Leu Pro Gly Leu Pro Gly Arg Asp Gly Val Pro Gly Leu Val Gly  
E--> 141 845 850 855  
142 Val Pro Gly Arg Pro Gly Val Arg Gly Leu Lys Gly Leu Pro Gly  
E--> 143 860 865 870  
144 Arg Asn Gly Glu Lys Gly Ser Gln Gly Phe Gly Tyr Pro Gly Glu  
E--> 145 875 880 885  
146 Gln Gly Pro Pro Gly Pro Pro Gly Pro Glu Gly Pro Pro Gly Ile

*same  
end*

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Input Set : A:\SEQUENCE LISTING.txt

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```

E--> 147      890      895      900
      148 Ser Lys Glu Gly Pro Pro Gly Asp Pro Gly Leu Pro Gly Lys Asp
E--> 149      905      910      915
      150 Gly Asp His Gly Lys Pro Gly Ile Gln Gly Gln Pro Gly Pro Pro
E--> 151      920      925      930
      152 Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser Val Ile Ala Arg Arg
E--> 153      935      940      945
      154 Asp Pro Phe Arg Lys Gly Pro Asn Tyr
E--> 155      950      954
      157 <210> SEQ ID NO: 2
      158 <211> LENGTH: 171
      159 <212> TYPE: PRT
      160 <213> ORGANISM: Homo sapiens
      162 <220> FEATURE:
      163 <223> OTHER INFORMATION: von Willebrand factor A domain
      165 <400> SEQUENCE: 2
      166 Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser Val Gly Pro Glu
E--> 167 1   5       10       15
      168 Asn Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile Thr Lys Asn
E--> 169 20      25       30
      170 Phe Asp Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val Gln Tyr
E--> 171 35      40       45
      172 Ser Asp Tyr Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp Ser
E--> 173 50      55       60
      174 Gly Glu His Leu Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly
E--> 175 65      70       75
      176 Gly Asn Thr Lys Thr Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr
E--> 177 80      85       90
      178 Leu Phe Ala Lys Ser Ser Arg Phe Leu Thr Lys Ile Ala Val Val
E--> 179 95      100      105
      180 Leu Thr Asp Gly Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln
E--> 181 110     115     120
      182 Ala Ala Arg Asp Ser Lys Ile Thr Leu Phe Ala Ile Gly Val Gly
E--> 183 125     130     135
      184 Ser Glu Thr Glu Asp Ala Glu Leu Arg Ala Ile Ala Asn Lys Pro
E--> 185 140     145     150
      186 Ser Ser Thr Tyr Val Phe Tyr Val Glu Asp Tyr Ile Ala Ile Ser
E--> 187 155     160     165
      188 Lys Ile Arg Glu Val Met
E--> 189 170 171
      192 <210> SEQ ID NO: 3
      193 <211> LENGTH: 183
      194 <212> TYPE: PRT
      195 <213> ORGANISM: Homo sapiens
      197 <220> FEATURE:
      198 <223> OTHER INFORMATION: Thrombospondin N-terminal-like domain
      200 <400> SEQUENCE: 3
      201 Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn Lys Lys Val Lys
E--> 202 1   5       10       15

```

*same**same**same*

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Input Set : A:\SEQUENCE LISTING.txt

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```

203 Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys Gly Tyr Glu Val
E--> 204 20 25 30
205 Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser Asn Val Phe Pro
E--> 206 35 40 45
207 Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser Thr Gln Arg Phe
E--> 208 50 55 60
209 Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile Asp
E--> 210 65 70 75
211 Gly Arg Pro Gln Ile Ala Val Thr Leu Asn Gly Val Asp Lys Ile
E--> 212 80 85 90
213 Leu Leu Phe Thr Thr Thr Ser Val Ile Asn Gly Ser Gln Val Val
E--> 214 95 100 105
215 Thr Phe Ala Asn Pro Gln Val Lys Thr Leu Phe Asp Glu Gly Trp
E--> 216 110 115 120
217 His Gln Ile Arg Leu Leu Val Thr Glu Gln Asp Val Thr Leu Tyr
E--> 218 125 130 135
219 Ile Asp Asp Gln Gln Ile Glu Asn Lys Pro Leu His Pro Val Leu
E--> 220 140 145 150
221 Gly Ile Leu Ile Asn Gly Gln Thr Gln Ile Gly Lys Tyr Ser Gly
E--> 222 155 160 165
223 Lys Glu Glu Thr Val Gln Phe Asp Val Gln Lys Leu Arg Ile Tyr
E--> 224 170 175 180
225 Cys Asp Pro
E--> 226 183
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 509
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
234 <220> FEATURE:
235 <223> OTHER INFORMATION: collagenous domain
236 Pro in this sequence stands for hydroxyproline
238 <400> SEQUENCE: 4
239 Gly Lys Pro Gly Leu Gln Gly Pro Lys Gly Asp Pro Gly Leu Pro
E--> 240 1 5 10 15
241 Gly Asn Pro Gly Tyr Pro Gly Gln Pro Gly Gln Asp Gly Lys Pro
E--> 242 20 25 30
243 Gly Tyr Gln Gly Ile Ala Gly Thr Pro Gly Val Pro Gly Ser Pro
E--> 244 35 40 45
245 Gly Ile Gln Gly Ala Arg Gly Leu Pro Gly Tyr Lys Gly Glu Pro
E--> 246 50 55 60
247 Gly Arg Asp Gly Asp Lys Gly Asp Arg Gly Leu Pro Gly Phe Pro
E--> 248 65 70 75
249 Gly Leu His Gly Met Pro Gly Ser Lys Gly Glu Met Gly Ala Lys
E--> 250 80 85 90
251 Gly Asp Lys Gly Ser Pro Gly Phe Tyr Gly Lys Lys Gly Ala Lys
E--> 252 95 100 105
253 Gly Glu Lys Gly Asn Ala Gly Phe Pro Gly Leu Pro Gly Pro Ala
E--> 254 110 115 120
255 Gly Glu Pro Gly Arg His Gly Lys Asp Gly Leu Met Gly Ser Pro

```

*same**same*

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Input Set : A:\SEQUENCE LISTING.txt

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```

E--> 256   125       130   135
      257 Gly Phe Lys Gly Glu Ala Gly Ser Pro Gly Ala Pro Gly Gln Asp
E--> 258   140       145   150
      259 Gly Thr Arg Gly Glu Pro Gly Ile Pro Gly Phe Pro Gly Asn Arg
E--> 260   155       160   165
      261 Gly Leu Met Gly Gln Lys Gly Glu Ile Gly Pro Pro Gly Gln Gln
E--> 262   170       175   180
      263 Gly Lys Lys Gly Ala Pro Gly Met Pro Gly Leu Met Gly Ser Asn
E--> 264   185       190   195
      265 Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys
E--> 266   200       205       210
      267 Gly Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser Gly Leu Lys
E--> 268   215       220       225
      269 Gly Glu Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met
E--> 270   230       235   240
      271 Gly Leu Pro Gly Ile Gln Gly Lys Lys Gly Asp Lys Gly Asn Gln
E--> 272   245       250   255
      273 Gly Glu Lys Gly Ile Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln
E--> 274   260       265   270
      275 Gly Ile Pro Gly Gln Gln Gly Ile Gln Gly His His Gly Ala Lys
E--> 276   275       280       285
      277 Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Val Arg Gly Ala Ile
E--> 278   290       295   300
      279 Gly Ser Lys Gly Glu Ser Gly Val Asp Gly Leu Met Gly Pro Ala
E--> 280   305       310   315
      281 Gly Pro Lys Gly Gln Pro Gly Asp Pro Gly Pro Gln Gly Pro Pro
E--> 282   320       325   330
      283 Gly Leu Asp Gly Lys Pro Gly Arg Glu Phe Ser Glu Gln Phe Ile
E--> 284   335       340   345
      285 Arg Gln Val Cys Thr Asp Val Ile Arg Ala Gln Leu Pro Val Leu
E--> 286   350       355   360
      287 Leu Gln Ser Gly Arg Ile Arg Asn Cys Asp His Cys Leu Ser Gln
E--> 288   365       370   375
      289 His Gly Ser Pro Gly Ile Pro Gly Pro Pro Gly Pro Ile Gly Pro
E--> 290   380       385       390
      291 Glu Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Arg Asp Gly Val
E--> 292   395       400   405
      293 Pro Gly Leu Val Gly Val Pro Gly Arg Pro Gly Val Arg Gly Leu
E--> 294   410       415   420
      295 Lys Gly Leu Pro Gly Arg Asn Gly Glu Lys Gly Ser Gln Gly Phe
E--> 296   425       430   435
      297 Gly Tyr Pro Gly Glu Gln Gly Pro Pro Gly Pro Pro Gly Pro Glu
E--> 298   440       445   450
      299 Gly Pro Pro Gly Ile Ser Lys Glu Gly Pro Pro Gly Asp Pro Gly
E--> 300   455       460       465
      301 Leu Pro Gly Lys Asp Gly Asp His Gly Lys Pro Gly Ile Gln Gly
E--> 302   470       475   480
      303 Gln Pro Gly Pro Pro Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser
E--> 304   485       490       495

```

*Adm*



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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\05142002\I996611A.raw

305 Val Ile Ala Arg Arg Asp Pro Phe Arg Lys Gly Pro Asn Tyr  
E--> 306 500 505 509

*same*

## VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\05142002\I996611A.raw

L:29 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
M:332 Repeated in SeqNo=1  
L:167 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:202 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3  
M:332 Repeated in SeqNo=3  
L:240 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
M:332 Repeated in SeqNo=4